PRINTER RUSH (PTO ASSISTANCE)

Application :	09/721,4-	Examiner:	S. CHEN	GAU:	1648	
From:	R. MITCH	EU Location:	OC FMF FDC	Date:	10/20/05	
Tracking #: <u>EPM 09/721, 47</u> 9 Week Date: <u>5/9/05</u>						
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[RUSH] MESSAGE: ATTENTION CHIEF DRAFTS PERSON						
FIGS. 11C, 11F, 11G, 14D, 14E, 14G, 14H, 17C, 18B, 18E, 21I, 22E HAS DATE STAMP OVER DATA.						
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[XRUSH] RESPONSE : — SEE ATTACHMENTS						
- DRAWINGS QORRECTED						
INITIAL C. OZ						
NOTE: This form will be included as part of the official USPTO record, with the Response						

document coded as XRUSH. REV 10/04

- 662 TGCAATACGTGTGACCCAGACAGTCGATTTCAGCCTTGACCCTACCTTCACCATTGAG ACGTTATGCACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGATGGAAGTGGTAACTC
- ThrileTheLeuProGlnAspAleValSerArgThrGlnArgArgGlyArgThrGlyArg
 722 ACAATCACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGG
 TGTTAGTGCGAGGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCC
- GlyLysProGlyIleTyrArgPheValAlaProGlyGluArgProSerGlyMetPheAsp GGGAAGCCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGAC CCCTTCGGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTG

822 BGLI, 839 DRD1,

887 SACI,

GluThrThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAsp 902 GAGACTACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGTGCCAGGAC CTCTGATGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTG

937 SMAI XMAI.

991 STUI,

- SerGlnThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrVal
 1022 TCCCAGACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTG
 AGGGTCTGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCAC
 1075 DRA3,
- CysAlaArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArg
 1082 TGCGCTAGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGC
 ACGCGATCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCG
- LeulysProthrleuHisGlyProthrProleuLeuTyrArgLeuGlyAlaValGlnAsn
 1142 CTCAAGCCCACCCTCCATGGGCCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAAT
 GAGTTCGGGTGGGAGGTACCCGGTTGTGGGGGACGATATGTCTGACCCGCGACAAGTCTTA

1156 NCOI,

1236 BSPH1, 1240 DRD1, 1243 AVA3, 1251 EAG1 XMA3, 1256 DRD1,

GluValValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyr GAGGTCGTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTTGGCCGCGTAT CTCCAGCAGTGCTCGTGGACCCACGAGCAACCGCCGCAGGACCGACGAAACCGGCGCATA CysleuSerThrGlyCysValValIleValGlyArqValValLeuSerGlyLysProAla 1322 TGCCTGTCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCA ACGGACAGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGT

1375 NAEI.

IleIleProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSerGln ATCATACCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAG TAGTATGGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACCTTCTCACGAGAGTC

1391 DRD1,

- HisLeuProTyrlleGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeu
 CACTTACCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTC
 GTGAATGGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAG
- GlyLeuLeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsn
 GGCCTCCTGCAGACCGCGCTCCGGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAAC
 CCGGAGGACGTCTGGCGCAGGCCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTG

1508 PSTI, 1513 TTH3I,

TrpGlnLysLeuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGln 1562 TGGCAAAAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAA ACCGTTTTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTT

1571 XHOI, 1592 NDEI,

TyrleuAlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPhe 1622 TACTTGGCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTT ATGAACCGCCCGAACAGTTGCGACGACCATTGGGGCGGTAACGAAGTAACTACCGAAAA

1649 BSTE2,

ThiAlaAlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGly
1682 ACAGCTGCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGG
TGTCGACGACAGTGGTCGGGTGATTGGTGATCGGTTTGGGAGGAGAAGTTGTATAACCCC

1683 ALWN1 PVU2,

GlyTrpValAlaAlaGlnLeuAlaAlaProGlyAlaAlaThrAlaPheValGlyAlaGly
1742 GGGTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCCTTTGTGGGCGCTGGC
CCCACCCACCGACGGTCGAGCGGGGGCCACGGCGATGACGGAAACACCCGCGACCG

1800 ESP1,

LeuAlaGlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAla
1802 TTAGCTGGCGCCCCATCGGCAGTGTTGGACTGGGAAGGTCCTCATAGACATCCTTGCA
AATCGACCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGT

1808 KAS1 NARI,

GlyTyrGlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluVal 1862 GGGTATGGCGGGGGGGGGGGGGGGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTC CCCATACCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAG

- IleLeuArgLysSerArgArgPheAlaGlnAlaL uProValTrpAlaArgPr AspTyr ATCCTGCGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTAT TAGGACGCCTTCAGAGCCTCTAAGCGGGTCCGGACGGCCAAACCCGCGCCGGCCTGATA
 - 3149 ALWN1, 3170 EAG1 XMA3,
- AsnProProLeuValGluThrTrpLysLysProAspTyrGluProProValValHisGly
 3182 AACCCCCGGCTAGTGGAGAGCGTGGAAAAAGCCCGACTACGAACCACCTGTGGTCCATGGC
 TTGGGGGGGGGATCACCTCTGCACCTTTTTCGGGCTGATGCTTGGTGGACACCAGGTACCG
 - 3223 HGIE2, 3235 NCOI,
- CysProLeuProProProLysSerProProValProProProArgLysLysArgThrVal
 3242 TGCCCGCTTCCACCTCCAAAGTCCCCTCCTGTGCCTCCGCCTCGGAAGAAGCGGACGGTG
 ACGGCCGAAGGTGGAGGTTTCAGGGGGAGGACACGGAGGCGGAGCCTTCTTCGCCTGCCAC
- ValLeuThrGluSerThrLeuSerThrAlaLeuAlaGluLeuAlaThrArgSerPheGly
 3302 GTCCTCACTGAATCAACCCTATCTACTGCCTTGGCCGAGCTCGCCAGAAGCTTTGGC
 CAGGAGTGACTTAGTTGGGATAGATGACGGAACCGGCTCGAGCGGTGGTCTTCGAAACCG
 - 3338 SACI, 3352 HIND3,
- SerGlyCysProProAspSerAspAlaGluSerTyrSerSerMetProProLeuGluGly
 TCTGGCTGCCCCCCGACTCCGACGCTGAGTCCTATTCCTCCATGCCCCCCCTGGAGGGG
 AGACCGACGGGGGGGCTGAGGCTGCGACTCAGGATAAGGAGGTACGGGGGGGACCTCCCC
 - 3443 EAM11051,
- GluProGlyAspProAspLeuSerAspGlySerTrpSerThrValSerSerGluAlaAsn
 GAGCCTGGGGATCCGGATCTTAGCGACGGGTCATGGTCAACGGTCAGTAGTGAGGCCAAC
 CTCGGACCCCTAGGCCTAGAATCGCTGCCCAGTACCAGTTGCCAGTCATCACTCCGGTTG
 - 3490 BAMHI, 3491 BSAB1, 3493 BSPE1,
- AlaGluAspValValCysCysSerMetSerTyrSerTrpThrGlyAlaLeuValThrPro 3542 GCGGAGGATGTCGTGCTGCTCAATGTCTTACTCTTGGACAGGCGCACTCGTCACCCCG CGCCTCCTACAGCACGACGAGTTACAGAATGAGAACCTGTCCGCGTGAGCAGTGGGGC
 - 3595 DRA3,
- CysAlaAlaGluGluLysLeuProlleAsnAlaLeuSerAsnSerLeuLeuArgHis
 3602 TGCGCCGCGGAAGAACAGAAACTGCCCATCAATGCACTAAGCAACTCGTTGCTACGTCAC
 ACGCGGCGCCTTCTTGTCTTTGACGGGTAGTTACGTGATTCGTTGAGCAACGATGCAGTG
 - 3606 SAC2, 3617 ALWN1, 3661 PFLM1.
- HisAsnLeuValTyrSerThrThrSerArgSerAlaCysGlnArgGlnLysLysValThr
 3662 CACAATTTGGTGTATTCCACCACCTCACGCAGTGCTTGCCAAAGGCAGAAGGAAAGTCACA
 GTGTTAAACCACATAAGGTGGTGGAGTGCGTCACGAACGGTTTCCGTCTTCTTTCAGTGT
 - 3687 DRA3,
 - PheAspArgLeuGlnValLeuAspSerHisTyrGlnAspValLeuLysGluValLysAla

- TTTGACAGACTGCAAGTTCTGGACAGCCATTACCAGGACGTACTCAAGGAGGTTAAAGCA AAACTGTCTGACGTTCAAGACCTGTCGGTAATGGTCCTGCATGAGTTCCTCCAATTTCGT AlaAlaSerLysValLysAlaAsnLeuLeuSerValGluGluAlaCysSerLeuThrPro GCGGCGTCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCC 3782 CGCCGCAGTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGG 3822 HIND3. ProHisSerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArg CCACACTCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGA GGTGTGAGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCT 3881 AAT2, 3896 BGLI, LysAlaValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrPro AAGGCCGTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCA TTCCGGCATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGT ${\tt IleAspThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGly}$ 3962 ATAGACACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGGT TATCTGTGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCA ArgLysProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMet CGTAAGCCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATG GCATTCGGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTAC AlaLeuTyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPhe GCTTTGTACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTC CGAAACATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAG GlnTyrSerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThr CAATACTCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACC GTTATGAGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGG 4166 ECORI, ProMetGlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIle 4202 CCAATGGGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATC GGTTACCCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAG 4235 DRD1, 4242 ALWN1, ArgThrGluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIle CGTACGGAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATC 4262 GCATGCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAG 4307 BGLI, 4314 BALI, LysSerLeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsn AAGTCCCTCACCGAGAGGCTTTATGTTGGGGGGCCCTCTTACCAATTCAAGGGGGGAGAAC TTCAGGGAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCTCTTG
- CysGlyTyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeu
 4382 TGCGGCTATCGCAGGTGCCGCGCGCGCGCGTACTGACAACTAGCTGTGGTAACACCCTC

4351 APAI,

- ThrGluAspLeuValAsnLeuLeuProAlaIl LeuSerProGlyAlaLeuValValGly
 1922 ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC
 TGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG
 1928 TTH31,
- ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGGAGTGCAGTGG CACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGTCACC

2004 NAEI, 2017 SMAI XMAI,

- MetAsnArgLeulleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal
 ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTG
 TACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCAC
 - 2067 SMAI XMAI, 2093 DRA3,
- ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln
 CCGGAGAGCGATGCAGCTGCCGCGTCACTGCCATACTCAGCAGCCTCACTGTAACCCAG
 GGCCTCTCGCTACGTCGACGGGCGCAGTGACGGTATGAGTCGTCGGAGTGACATTGGGTC
 - 2115 PVU2, 2159 ALWN1,
- LeuLeuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer 2162 CTCCTGAGGCGACCAGGGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG
 - 2164 MST2, 2220 ECON1,
- TrpLeuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu 2222 TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA ACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGAT
- LysGlyValTrpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle 2342 AAGGGGTCTGGCGAGGGGACGGCATCATGCACACTCGCTGCCACTGTGGAGCTGAGATC TTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG
- ThrGlyHisValLysAsnGlyThrMetArglleValGlyProArgThrCysArgAsnMet
 ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATG
 TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCAGGATCCTGGACGTCCTTGTAC
 - 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,
- TrpSerGlyThrPheProlleAsnAlaTyrThrThrGlyProCysThrProLeuProAla 2462 TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCG ACCTCACCCTGGAAGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC
 - 2480 ASE1, 2497 APAI,
 - ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln

- ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln
 2582 GTGGGGGACTTCCACTACGTGACGGGTATGACTGACAATCTTAAATGCCCGTGCCAG
 CACCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC
- ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro 2642 GTCCCATCGCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC CAGGGTAGCGGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG
- ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
 CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG
 GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC

2757 HGIE2,

2594 DRA3,

ValGlySerGlnLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
2762 GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC
CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG

2809 AAT2,

ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
2022 ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCC
TGACTAGGGAGGGTATATTGTCGTCTCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG

2850 EAG1 XMA3,

ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG

2889 BALI, 2903 NHEI,

ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
2942 ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG
TGGCGATTGGTACTGAGGGGACTACGACTCGAGTATCTCCGGTTGGAGGATACCTCCGTC

2966 ESP1, 2969 SACI,

- GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer
 3002 GAGATGGGCGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC
 CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG
- PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
 TTCGATCCGCTTGTGGCGGAGGAGGACGCGGGGGGAGATCTCCGTACCCGCAGAAATCCTG
 AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC

3096 BGL2.

ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro 3122 CGGAAGTCTCGGAGATTCGCCCAGGCCCTGCCCGTTTGGGCGCGGCCGGACTATAACCCC

3782	TCAAAAGTGAAGGCTAACTTGCTATCCGTAGAGGAAGCTTGCAGCCTGACGCCCCCACAC AGTTTTCACTTCCGATTGAACGATAGGCATCTCCTTCGAACGTCGGACTGCGGGGGTGTG
	3816 HIND3,
3842	SerAlaLysSerLysPheGlyTyrGlyAlaLysAspValArgCysHisAlaArgLysAla TCAGCCAAATCCAAGTTTGGTTATGGGGCAAAAGACGTCCGTTGCCATGCCAGAAAGGCC AGTCGGTTTAGGTTCAAACCAATACCCCGTTTTCTGCAGGCAACGGTACGGTCTTTCCGG
	3875 AAT2, 3890 BGLI,
3902	ValThrHisIleAsnSerValTrpLysAspLeuLeuGluAspAsnValThrProIleAsp GTAACCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAATGTAACACCAATAGAC CATTGGGTGTAGTTGAGGCACACCTTTCTGGAAGACCTTCTGTTACATTGTGGTTATCTG
3962	ThrThrIleMetAlaLysAsnGluValPheCysValGlnProGluLysGlyGlyArgLys ACTACCATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGGTCGTAAG TGATGGTAGTACCGATTCTTGCTCCAAAAGACGCAAGTCGGACTCTTCCCCCCAGCATTC
1022	ProAlaArgLeuIleValPheProAspLeuGlyValArgValCysGluLysMetAlaLeu CCAGCTCGTCTCATCGTGTTCCCCGATCTGGGCGTGCGCGTGTGCGAAAAGATGGCTTTG GGTCGAGCAGAGTAGCACAAGGGGCTAGACCCGCACGCGCACACGCTTTTCTACCGAAAC
1082	TyrAspValValThrLysLeuProLeuAlaValMetGlySerSerTyrGlyPheGlnTyr TACGACGTGGTTACAAAGCTCCCCTTGGCCGTGATGGGAAGCTCCTACGGATTCCAATAC ATGCTGCACCAATGTTTCGAGGGGAACCGGCACTACCCTTCGAGGATGCCTAAGGTTATG
4142	SerProGlyGlnArgValGluPheLeuValGlnAlaTrpLysSerLysLysThrProMet TCACCAGGACAGCGGGTTGAATTCCTCGTGCAAGCGTGGAAGTCCAAGAAAACCCCAATG AGTGGTCCTGTCGCCCAACTTAAGGAGCACGTTCGCACCTTCAGGTTCTTTTGGGGTTAC
	4160 ECORI,
1202	GlyPheSerTyrAspThrArgCysPheAspSerThrValThrGluSerAspIleArgThr GGGTTCTCGTATGATACCCGCTGCTTTGACTCCACAGTCACTGAGAGCGACATCCGTACG CCCAAGAGCATACTATGGGCGACGAAACTGAGGTGTCAGTGACTCTCGCTGTAGGCATGC
	4229 DRD1, 4236 ALWN1,
1262	GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer GAGGAGGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGGTTCGGGCGCACCGGTAGTTCAGG
	4301 BGLI, 4308 BALI,
1322	LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGlyCTCACCGAGAGGCTTTATGTTGGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGCGAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCCTCTTGACGCCG
	4345 APAI,
1382	TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys TATCGCAGGTGCCGCGGGGGGGGGTACTGACAACTAGCTGTGGTAACACCCTCACTTGC ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTTGATCGACACCATTGTGGGAGTGAACG

TyrilelysklakrgklaklaCyskrgklaklaGlyLeuGlnAspCysThrMetLeuVal TACATCAAGGCCCGGGCAGCCTGTCGAGCCCAGGGCTCCAGGACTGCACCATGCTCGTG ATGTAGTTCCGGGCCCGTCGGACAGCTCGGCGTCCCGAGGTCCTGACGTGCTACGAGCAC

4452 SMAI KMAI,

CysGlyAspAspLeuValVallleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
4502 TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGGGGCGAGC
ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCCAGGTCCTCCTGCGCCGCTCG

4508 DRD1, 4511 TTH31,

- LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
 4562 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCTGGGGACCCCCCACAA
 GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGACCCCTGGGGGGTGTT
- ProGlutyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp
 4622 CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC
 GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG

4637 SACI,

GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla
4682 GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCCTACAACCCCCCTCGCGAGAGCT
CCGCGACCTTTCTCCCAGATGATGGAGTGGGCACTGGGATGTTGGGGGGGAGCGCTCTCGA

4731 NRUI,

- AlatrpGluthrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe GCGTGGGAGACAGCAAGACACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT CGCACCCTCTGTCGTTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA
- AlaProThrLeuTrpAlaArgMetIleLeuMetThrHisPhePheSerValLeuIleAla GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG

4806 PFLM1, 4807 DRA3,

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu 4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT

4893 BGL2,

ProLeuAspleuProProlleTleGlnArgLeuHisGlyLeuSerAlaPheSerLeuHis
4922 CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG

4954 NCOI,

SerTyrSerProGlyGlulleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC

5015 SPHI, 5035 KPNI,

ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly

TCCCGAGTTCGGGGAGGGGGTAGCACCTTGGTCTACACCTTCACAAACTAAGCGGAGTTC

- ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
 1142 CCCACCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC
 GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG
 1150 NCOI.
- - 1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,
- ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu 1262 GTCACGAGCACCTGGGTGCTCGTTGGCGGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTG CAGTGCTCGTGGACCCACGAGCCACCGCCGCAGAACCGGCGCATAACGGAC
- SerThrGlyCysValValIleValGlyArgValValLeuSerGlyLysProAlaileIle
 1322 TCAACAGGCTGCGTGGTCATAGTGGGCAGGGTCGTCTTGTCCGGGAAGCCGGCAATCATA
 AGTTGTCCGACGCACCAGTATCACCCGTCCCAGCAGAACAGGCCCTTCGGCCGTTAGTAT
 1369 NAEI.
- ProAspArgGluValLeuTyrArgGluPheAspGluMetGluGluCysSergInHisLeu
 1382 CCTGACAGGGAAGTCCTCTACCGAGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTA
 GGACTGTCCCTTCAGGAGATGGCTCTCAAGCTACTCTCACGAGAGTCGTGAAT
 1385 DRD1.
- ProTyrileGluGlnGlyMetMetLeuAlaGluGlnPheLysGlnLysAlaLeuGlyLeu
 1442 CCGTACATCGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTC
 GGCATGTAGCTCGTTCCCTACTACGAGCGGCTCGTCAAGTTCGTCTTCCGGGAGCCGGAG
- LeuGlnThrAlaSerArgGlnAlaGluValIleAlaProAlaValGlnThrAsnTrpGln
 CTGCAGACCGCGTCCGGTCAGGCAGAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAA
 GACGTCTGGCGCAGGGCAGTCCGTCTCCAATAGCGGGGACGACAGGTCTGGTTGACCGTT

 1502 PSTI, 1507 TTH31.
- LysleuGluThrPheTrpAlaLysHisMetTrpAsnPheIleSerGlyIleGlnTyrLeu
 AAACTCGAGACCTTCTGGGCGAAGCATATGTGGAACTTCATCAGTGGGATACAATACTTG
 TTTGAGCTCTGGAAGACCCGCTTCGTATACACCTTGAAGTAGTCACCCTATGTTATGAAC
 1565 XHOI, 1586 NDEI.
- AlaGlyLeuSerThrLeuProGlyAsnProAlaIleAlaSerLeuMetAlaPheThrAla GCGGGCTTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTACAGCT CGCCCGAACAGTTGCGACGGACCATTGGGGCGGTAACGAAGTAACTACCGAAAATGTCGA
 - 1643 BSTE2, 1677 ALWN1 PVU2,
- AlaValThrSerProLeuThrThrSerGlnThrLeuLeuPheAsnIleLeuGlyGlyTrp
 1682 GCTGTCACCAGCCCACTAACCACTAGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGG
 CGACAGTGGTCGGTGATTGGTGATCGGTTTGGGAGGAGAGTTGTATAACCCCCCCACC

- ValalaalaGlnLeualaalaPr GlyalaalaThrAlaPheValGlyAlaGlyLeuala 1742 GTGGCTGCCCAGCTCGCCGCCCCCGGTGCCGCTACTGCTTTGTGGGCGCTGGCTTAGCT CACCGACGGGTCGAGCGGGGGGCCACGGCGATGACGGAAACACCCCGCGACCGAATCGA
 - 1794 ESP1,
- GlyAlaAlaIleGlySerValGlyLeuGlyLysValLeuIleAspIleLeuAlaGlyTyr
 GGCGCCGCCATCGGCAGTGTTGGACTGGGGAAGGTCCTCATAGACATCCTTGCAGGGTAT
 CCGCGGCGGTAGCCGTCACAACCTGACCCCTTCCAGGAGTATCTGTAGGAACGTCCCATA
 1802 KAS1 NARI.
- GlyAlaGlyValAlaGlyAlaLeuValAlaPheLysIleMetSerGlyGluValProSer GGCGCGGGCGTGGCGGGAGCTCTTGTGGCATTCAAGATCATGAGCGGTGAGGTCCCCTCC CCGCGCCCGCACCGCCCTCGAGAACACCGTAAGTTCTAGTACTCGCCACTCCAGGGGAGG
 - 1878 SACI, 1899 BSPH1,
- ThrGluAspLeuValAsnLeuLeuProAlaIleLeuSerProGlyAlaLeuValValGly
 1922 ACGGAGGACCTGGTCAATCTACTGCCCGCCATCCTCTCGCCCGGAGCCCTCGTAGTCGGC
 TGCCTCCTGGACCAGTTAGATGACGGGCGGTAGGAGAGCGGGCCTCGGGAGCATCAGCCG
 1928 TTH31.
- ValValCysAlaAlaIleLeuArgArgHisValGlyProGlyGluGlyAlaValGlnTrp GTGGTCTGTGCAGCAATACTGCGCCGGCACGTTGGCCCGGGCGAGGGGGCAGTGCAGTGG CACCAGACACGTCGTTATGACGCGGCCGTGCAACCGGGCCCGCTCCCCCGTCACGTCACC
 - 2004 NAEI, 2017 SMAI XMAI,
- MetAsnArgLeulleAlaPheAlaSerArgGlyAsnHisValSerProThrHisTyrVal
 ATGAACCGGCTGATAGCCTTCGCCTCCCGGGGGAACCATGTTTCCCCCACGCACTACGTG
 TACTTGGCCGACTATCGGAAGCGGAGGGCCCCCTTGGTACAAAGGGGGTGCGTGATGCAC
 - 2067 SMAI XMAI, 2093 DRA3,
- ProGluSerAspAlaAlaAlaArgValThrAlaIleLeuSerSerLeuThrValThrGln
 CCGGAGAGCGATGCAGCTGCCCGCGTCACTGCATCTCAGCAGCCTCACTGTAACCCAG
 GGCCTCTCGCTACGTCGACGGCGCAGTGACGTTATGAGTCGTCGGAGTGACATTGGGTC
 - 2115 PVU2, 2159 ALWN1,
- LeuleuArgArgLeuHisGlnTrpIleSerSerGluCysThrThrProCysSerGlySer
 CTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGTACCACTCCATGCTCCGGTTCC
 GAGGACTCCGCTGACGTGGTCACCTATTCGAGCCTCACATGGTGAGGTACGAGGCCAAGG
 - 2164 MST2, 2220 ECON1,
- TrpleuArgAspIleTrpAspTrpIleCysGluValLeuSerAspPheLysThrTrpLeu
 TGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGTTGAGCGACTTTAAGACCTGGCTA
 ACCGATTCCCTGTAGACCCTGACCTATACGCTCCACAACTCGCTGAAATTCTGGACCGAT
- - 2285 ESP1, 2300 PVU2, 2310 BAMHI,

- ThrCysValThrGlnThrValAspPheSerLeuAspPr ThrPheThrIleGluThrIle ACGTGTGTCACCCAGACAGTCGATTTCAGCCTTGACCCTACCCTTCACCATTGAGACAATC TGCACAGTGGGTCTGTCAGCTAAAGTCGGAACTGGGAAGTGGTAACTCTGTTAG
- ThrLeuProGlnAspAleValSerArgThrGlnArgArgGlyArgThrGlyArgGlyLys
 ACGCTCCCCCAAGATGCTGTCTCCCGCACTCAACGTCGGGGCAGGACTGGCAGGGGGAAG
 TGCGAGGGGGTTCTACGACAGAGGGCGTGAGTTGCAGCCCCGTCCTGACCGTCCCCCTTC
- ProglylleTyrArgPheValAlaProglyGluArgProSerGlyMetPheAspSerSer
 CCAGGCATCTACAGATTTGTGGCACCGGGGGAGCGCCCCTCCGGCATGTTCGACTCGTCC
 GGTCCGTAGATGTCTAAACACCGTGGCCCCCTCGCGGGGAGGCCGTACAAGCTGAGCAGG

816 BGLI, 833 DRD1,

881 SACI,

ThrValArgLeuArgAlaTyrMetAsnThrProGlyLeuProValCysGlnAspHisLeu
902 ACAGTTAGGCTACGAGCGTACATGAACACCCCGGGGCTTCCCGTGGCCAGGACCATCTT
TGTCAATCCGATGCTCGCATGTACTTGTGGGGCCCCGAAGGGCACACGGTCCTGGTAGAA

931 SMAI XMAI,

GluPheTrpGluGlyValPheThrGlyLeuThrHisIleAspAlaHisPheLeuSerGln 962 GAATTTTGGGAGGGCGTCTTTACAGGCCTCACTCATATAGATGCCCACTTTCTATCCCAG CTTAAAACCCTCCCGCAGAAATGTCCGGAGTGAGTATATCTACGGGTGAAAGATAGGGTC

985 STUI,

ThrLysGlnSerGlyGluAsnLeuProTyrLeuValAlaTyrGlnAlaThrValCysAla ACAAAGCAGAGTGGGGAGAACCTTCCTTACCTGGTAGCGTACCAAGCCACCGTGTGCGCT TGTTTCGTCTCACCCCTCTTGGAAGGAATGGACCATCGCATGGTTCGGTGGCACACGCGA

1069 DRA3,

- ArgAlaGlnAlaProProProSerTrpAspGlnMetTrpLysCysLeuIleArgLeuLys
 AGGGCTCAAGCCCCTCCCCCATCGTGGGACCAGATGTGGAAGTGTTTGATTCGCCTCAAG
 TCCCGAGTTCGGGGAGGGGGTAGCACCCTGGTCTACACCTTCACAAACTAAGCGGAGTTC
- ProThrLeuHisGlyProThrProLeuLeuTyrArgLeuGlyAlaValGlnAsnGluIle
 CCCACCTCCATGGGCCAACACCCCTGCTATACAGACTGGGCGCTGTTCAGAATGAAATC
 GGGTGGGAGGTACCCGGTTGTGGGGACGATATGTCTGACCCGCGACAAGTCTTACTTTAG

 1150 NCOI.

1230 BSPH1, 1234 DRD1, 1237 AVA3, 1245 EAG1 XMA3, 1250 DRD1,

ValThrSerThrTrpValLeuValGlyGlyValLeuAlaAlaLeuAlaAlaTyrCysLeu 1262 GTCACGAGCACCTGGGTGCTCGTTGGCCGCGTCCTGGCTGCTTTGGCCGCGTATTGCCTG

- ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
 CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
 GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
 2553 PSTI,
- ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG CACCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC 2594 DRA3.
- ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro GTCCCATCGCCCGAATTTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG
- ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro
 CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG
 GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
 2757 HGIE2.
- ValGlySerGinLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu
 GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACCGTGTGACGTCCATGCTC
 CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG
 2809 AAT2.
- ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
 ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGGCGAAGGTTGGCGAGGGGATCACCC
 TGACTAGGGAGGGTATATTGTCGTCTCCCGCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG
 2850 EAGl XMA3.
- ProSerValAlaSerSerSerAlaSerGlnLeuSerAlaProSerLeuLysAlaThrCys
 CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
 GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
 2889 BALI, 2903 NHEI.
- ThrAlaAsnHisAspSerProAspAlaGluLeuIleGluAlaAsnLeuLeuTrpArgGln
 ACCGCTAACCATGACTCCCCTGATGCTGAGCTCATAGAGGCCAACCTCCTATGGAGGCAG
 TGGCGATTGGTACTGAGGGGACTACGACTCCGGTTTGGAGGATACCTCCGTC
 2966 ESP1, 2969 SACI.
- GluMetGlyGlyAsnIleThrArgValGluSerGluAsnLysValValIleLeuAspSer 3002 GAGATGGGCGCAACATCACCAGGGTTGAGTCAGAAAACAAAGTGGTGATTCTGGACTCC CTCTACCCGCCGTTGTAGTGGTCCCAACTCAGTCTTTTGTTTCACCACTAAGACCTGAGG
- PheAspProLeuValAlaGluGluAspGluArgGluIleSerValProAlaGluIleLeu
 TTCGATCCGCTTGTGGCGGAGGAGGACGACGGGGGAGATCTCCGTACCCGCAGAAATCCTG
 AAGCTAGGCGAACACCGCCTCCTCCTGCTCGCCCTCTAGAGGCATGGGCGTCTTTAGGAC
 3096 BGL2.

ArgLysSerArgArgPheAlaGlnAlaLeuProValTrpAlaArgProAspTyrAsnPro

- ProleuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
 5042 CCCTTGCGAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGGCCTAGGCTTCTGGCCAGAGCGCGGGCCCCGGGCGCGATCCGAAGACCGGTCTCCT
 - 5064 APAI, 5091 BALI.
- GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys 5102 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA CCGTCCCGACGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT
 - 5113 NDEI,
- - 5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,
- SerglyGlyAspIleTyrHisSerValSerHisAlaArgProArgTrpIleTrpPheCys
 AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC
 TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGCGACCTAGACCAAAACG
 - 5240 DRA3,
- LeuleuleuleuAlaAlaGlyValGlyIleTyrLeuleuProAsnArgMetSerThrAsn 5282 CTACTCCTGCTTGCTGCAGGGGTAGGCATCTACCTCCTCCCCAACCGAATGAGCACGAAT GATGAGGACGAACGACGTCCCCATCCGTAGATGGAGGAGGGGTTGGCTTACTCGTGCTTA
 - 5295 PSTI.
- ProlysproglnArglysThrLysArgAsnThrAsnArgArgProglnAspVallysPhe
 5342 CCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGGGGGCGCGCAGGACGTCAAGTTC
 GGATTTGGAGTTCTTCTTGGTTTGCATTGTGGTTGGCCGCGGGGTCCTGCAGTTCAAG
 - 5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,
- ProGlyGlyGlnileValGlyGlyValTyrLeuLeuProArgArgGlyProArgLeu
 5402 CCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTG
 GGCCCACCGCCAGTCTAGCAACCACCTCAAATGAACAACGGCGCGTCCCCGGGATCTAAC
 - 5.449 APAI,
- GlyValArgAlaThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro
 5462 GGTGTGCGCGACGAGAAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCT
 CCACACGCGCGCGCTGCTCTTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGA
 - 5467 BSSH2, 5478 XMNI, 5502 XHOI, 5511 AAT2,
- IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGlyTyrProTrpPro
 ATCCCAAGGCTCGTCGGCCCGAGGGCAGGCCTGGGCTCAGCCCGGGTACCCTTGGCCC
 TAGGGGTTCCGAGCAGCCGGGCTCCCGTCCTGGACCCGAGTCGGGCCCATGGGAACCGGG
 - 5548 ALWN1, 5558 ESP1, 5564 SMAI XMAI, 5568 KPNI,
- LeutyrGlyAsnGluGlyCysGlyTrpAlaGlyTrpLeuLeuSerProArgGlySerArg
 5582 CTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGGCTCTCGG
 GAGATACCGTTACTCCCGACGCCCCACCCGCCCTACCGAGGACAGAGGGGCACCGAGAGCC

4229 DRD1, 4236 ALWN1,

GluGluAlaIleTyrGlnCysCysAspLeuAspProGlnAlaArgValAlaIleLysSer 4262 GAGGAGCAATCTACCAATGTTGTGACCTCGACCCCCAAGCCCGCGTGGCCATCAAGTCC CTCCTCCGTTAGATGGTTACAACACTGGAGCTGGGGGTTCGGGCGCACCGGTAGTTCAGG

4301 BGLI, 4308 BALI,

LeuThrGluArgLeuTyrValGlyGlyProLeuThrAsnSerArgGlyGluAsnCysGly
4322 CTCACCGAGAGGCTTTATGTTGGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGCGGC
GAGTGGCTCTCCGAAATACAACCCCCGGGAGAATGGTTAAGTTCCCCCCCTCTTGACGCCG

4345 APAI,

- TyrArgArgCysArgAlaSerGlyValLeuThrThrSerCysGlyAsnThrLeuThrCys
 4382 TATCGCAGGTGCCGCGGGGGGGGGGTACTGACACTAGCTGTGGTAACACCCTCACTTGC
 ATAGCGTCCACGGCGCGCTCGCCGCATGACTGTGATCGACACCATTGTGGGAGTGAACG
- TyrilelysAlaArgAlaAlaCysArgAlaAlaGlyLeuGlnAspCysThrMetLeuVal
 4442 TACATCAAGGCCCGGGCAGCCTGTCGAGGCCGCAGGGCTCCAGGACTGCACCATGCTCGTG
 ATGTAGTTCCGGGCCCGTCGGACAGCTCCGGCGTCCCGAGGTCCTGACGTGCTACGAGCAC

4452 SMAI XMAI,

- CysGlyAspAspLeuValVallleCysGluSerAlaGlyValGlnGluAspAlaAlaSer
 4502 TGTGGCGACGACTTAGTCGTTATCTGTGAAAGCGCGGGGGTCCAGGAGGACGCGGCGAGC
 ACACCGCTGCTGAATCAGCAATAGACACTTTCGCGCCCCCAGGTCCTCCTGCGCCGCTCG
 4508 DRD1, 4511 TTH31.
- LeuArgAlaPheThrGluAlaMetThrArgTyrSerAlaProProGlyAspProProGln
 CTGAGAGCCTTCACGGAGGCTATGACCAGGTACTCCGCCCCCCTGGGGACCCCCCACAA
 GACTCTCGGAAGTGCCTCCGATACTGGTCCATGAGGCGGGGGGGACCCCTGGGGGGTGTT
- ProGlutyrAspLeuGluLeuIleThrSerCysSerSerAsnValSerValAlaHisAsp CCAGAATACGACTTGGAGCTCATAACATCATGCTCCTCCAACGTGTCAGTCGCCCACGAC GGTCTTATGCTGAACCTCGAGTATTGTAGTACGAGGAGGTTGCACAGTCAGCGGGTGCTG 4637 SACI.
- GlyAlaGlyLysArgValTyrTyrLeuThrArgAspProThrThrProLeuAlaArgAla GGCGCTGGAAAGAGGGTCTACTACCTCACCCGTGACCCTACAACCCCCCTCGCGAGAGCT CCGCGACCTTTCTCCCAGATGATGGAGTGGCCACTGGGATGTTGGGGGGGAGCGCTCTCGA

4731 NRUI.

- AlatrpGluThrAlaArgHisThrProValAsnSerTrpLeuGlyAsnIleIleMetPhe 4742 GCGTGGGAGACAGCAAGACACTCCAGTCAATTCCTGGCTAGGCAACATAATCATGTTT CGCACCCTCTGTCGTTCTGTGTGAGGTCAGTTAAGGACCGATCCGTTGTATTAGTACAAA
- AleprothrleutrpaleargmetileLeuMetthrHisPhePheSerValLeuIleale GCCCCCACACTGTGGGCGAGGATGATACTGATGACCCATTTCTTTAGCGTCCTTATAGCC CGGGGGTGTGACACCCGCTCCTACTATGACTACTGGGTAAAGAAATCGCAGGAATATCGG

4806 PFLM1, 4807 DRA3,

ArgAspGlnLeuGluGlnAlaLeuAspCysGluIleTyrGlyAlaCysTyrSerIleGlu

- 4862 AGGGACCAGCTTGAACAGGCCCTCGATTGCGAGATCTACGGGGCCTGCTACTCCATAGAA
 TCCCTGGTCGAACTTGTCCGGGAGCTAACGCTCTAGATGCCCCGGACGATGAGGTATCTT
 4893 BGL2,
- ProLeuAspleuProProllelleGlnArgleuHisGlyLeuSerAlaPheSerLeuHis
 4922 CCACTGGATCTACCTCCAATCATTCAAAGACTCCATGGCCTCAGCGCATTTTCACTCCAC
 GGTGACCTAGATGGAGGTTAGTAAGTTTCTGAGGTACCGGAGTCGCGTAAAAGTGAGGTG
 4954 NCOI,
- SerTyrSerProGlyGluIleAsnArgValAlaAlaCysLeuArgLysLeuGlyValPro AGTTACTCTCCAGGTGAAATCAATAGGGTGGCCGCATGCCTCAGAAAACTTGGGGTACCG TCAATGAGAGGTCCACTTTAGTTATCCCACCGGCGTACGGAGTCTTTTGAACCCCATGGC

5015 SPHI, 5035 KPNI,

ProLeuArgAlaTrpArgHisArgAlaArgSerValArgAlaArgLeuLeuAlaArgGly
CCCTTGCGAGCTTGGAGACACCGGGCCCGGGCCTCGCAGGCGTCCGAAGACCGGTCTCCT
GGGAACGCTCGAACCTCTGTGGCCCGGGCCTCGCAGGCGCGATCCGAAGACCGGTCTCCT

5064 APAI, 5091 BALI,

- GlyArgAlaAlaIleCysGlyLysTyrLeuPheAsnTrpAlaValArgThrLysLeuLys
 GGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAA
 CCGTCCCGACGGTATACACCGTTCATGGAGAAGTTGACCCGTCATTCTTGTTTCGAGTTT

 5113 NDEI.

5174 NOTI, 5175 EAG1 XMA3, 5182 BALI, 5186 PVU2,

- SerGlyGlyAsplleTyrHisSerValSerHisAlaArgProArgTrplleTrpPheCys
 5222 AGCGGGGGAGACATTTATCACAGCGTGTCTCATGCCCGGCCCCGCTGGATCTGGTTTTGC
 TCGCCCCCTCTGTAAATAGTGTCGCACAGAGTACGGGCCGGGCGACCTAGACCAAAACG
 5240 DRA3,

5380 NOTI, 5381 EAG1 XMA3, 5390 AAT2, 5401 SMAI XMAI,

^^

- LysGlyValTzpArgGlyAspGlyIleMetHisThrArgCysHisCysGlyAlaGluIle
 2342 AAGGGGTCTGGCGAGGGGACGCCATCATGCACACTCGCTGCCACTGTGGAGCTCAGATC
 TTCCCCCAGACCGCTCCCCTGCCGTAGTACGTGTGAGCGACGGTGACACCTCGACTCTAG
- ThrGlyHisVallysAsnGlyThrMetArgIleValGlyProArgThrCysArgAsnMet
 ACTGGACATGTCAAAAACGGGACGATGAGGATCGTCGGTCCTAGGACCTGCAGGAACATG
 TGACCTGTACAGTTTTTGCCCTGCTACTCCTAGCAGCCCAGGATCCTGGACGTCCTTGTAC
 - 2425 BSAB1, 2441 AVR2, 2448 SSE83871, 2449 PSTI,
- TrpSerGlyThrPheProIleAsnAlaTyrThrThrGlyProCysThrProLeuProAla
 TGGAGTGGGACCTTCCCCATTAATGCCTACACCACGGGCCCCTGTACCCCCCTTCCTGCG
 ACCTCACCCTGGAAGGGGGTAATTACGGATGTGGTGCCCGGGGACATGGGGGGAAGGACGC
 - 2480 ASE1, 2497 APAI,
- ProAsnTyrThrPheAlaLeuTrpArgValSerAlaGluGluTyrValGluIleArgGln
 CCGAACTACACGTTCGCGCTATGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCAG
 GGCTTGATGTGCAAGCGCGATACCTCCCACAGACGTCTCCTTATGCACCTCTATTCCGTC
 - 2553 PSTI.
- ValGlyAspPheHisTyrValThrGlyMetThrThrAspAsnLeuLysCysProCysGln 2582 GTGGGGGACTTCCACTACGTGACGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAG CACCCCCTGAAGGTGATGCACTGCCCATACTGATGACTGTTAGAATTTACGGGCACGGTC
 - 2594 DRA3.
- ValProSerProGluPhePheThrGluLeuAspGlyValArgLeuHisArgPheAlaPro GTCCCATCGCCCGAATTTTCACAGAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCC CAGGGTAGCGGGCTTAAAAAGTGTCTTAACCTGCCCCACGCGGATGTATCCAAACGCGGG
- ProCysLysProLeuLeuArgGluGluValSerPheArgValGlyLeuHisGluTyrPro CCCTGCAAGCCCTTGCTGCGGGAGGAGGTATCATTCAGAGTAGGACTCCACGAATACCCG GGGACGTTCGGGAACGACGCCCTCCTCCATAGTAAGTCTCATCCTGAGGTGCTTATGGGC
 - 2757 HGIE2,
- ValGlySerGinLeuProCysGluProGluProAspValAlaValLeuThrSerMetLeu 2762 GTAGGGTCGCAATTACCTTGCGAGCCCGAACCGGACGTGGCCGTGTTGACGTCCATGCTC CATCCCAGCGTTAATGGAACGCTCGGGCTTGGCCTGCACCGGCACAACTGCAGGTACGAG
 - 2809 AAT2,
- ThrAspProSerHisIleThrAlaGluAlaAlaGlyArgArgLeuAlaArgGlySerPro
 2822 ACTGATCCCTCCCATATAACAGCAGAGGCGGCCGGCCGAAGGTTGGCGAGGGGATCACCC
 TGACTAGGGAGGGTATATTGTCGTCTCCCCCGGCCCGCTTCCAACCGCTCCCCTAGTGGG
 - 2850 EAG1 XMA3.
- ProserValAlaserSerSerAlaserGlnLeuserAlaProserLeuLysAlaThrCys
 2882 CCCTCTGTGGCCAGCTCCTCGGCTAGCCAGCTATCCGCTCCATCTCTCAAGGCAACTTGC
 GGGAGACACCGGTCGAGGAGCCGATCGGTCGATAGGCGAGGTAGAGAGTTCCGTTGAACG
 - 2889 BALI, 2903 NHEI,

FIG. 22E